Clone 40:

*GAATTCGGCACGAG*TCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT
GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
GATCGGGCTTTGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCAC
AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAAATTCTC
TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACC
AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
ATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAAAA
AAAAAAAAAAAAAA*CTCGAG*

Clone 3:

*GAATTCGGCACGAG*GGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT
GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAG
GATCGGGCTTTGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCAC
AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAAATTCTC
TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTTAT
TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
CTGGTAGATCTATCAGACCACTTTTATCAGCAGGACAACTGGTCGTTACC
AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
ATAGAATATTGAAAATAA

Clone 5:

*G*TCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTTGCTCTTGTCGCTCTATGCTTAATGCAACCGGG
TTCCGGTGAGGAAGTACAATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACTG
GATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAGGATCGGGCTTTGGGGCTGTG
TCGGATTGAACGGGCCGGCCCAGGTACCACAAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTC
ATGTGTAACAAGAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGACTACAGACC
ACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAAATTCTCTAGCAAAATGCCAGGCACTTACATGCT
TATGGACGTGTGCGCTACAAGGGACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAG
GGTGTCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTTATTCCATCTGAGACAAT
CGAGGATGATATCAAGGACTGTGGGCTCTTAGACCAAGATGTTGAACTCGATTATACGTGGACTCAAAA
CGAGTGTGATCTACCAGACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTTCTG
GTAGATCTATCAGACCACTTTTATCAGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCA
TCAATAATGTGTAAAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAGACACTGGTTGAA
AAAAAAAAAAAAAAAAAA*CTCGAG*

Fig. 1

```
clone 40     GAATTCGGCACGAGTCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT
clone 3      GAATTCGGCACGAG--GGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT
clone 5      -------------GTCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT
                          *  **********************************

clone 40     GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
clone 3      GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
clone 5      GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
             **************************************************

clone 40     ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
clone 3      ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
clone 5      ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
             **************************************************

clone 40     GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
clone 3      GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAG
clone 5      GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAG
             ************************************************* 

clone 40     GATCGGGCTTTGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCAC
clone 3      GATCGGGCTTTGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCAC
clone 5      GATCGGGCTTTGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCAC
             **************************************************

clone 40     AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
clone 3      AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
clone 5      AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
             **************************************************

clone 40     GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
clone 3      GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
clone 5      GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
             **************************************************

clone 40     TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC
clone 3      TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC
clone 5      TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC
             **************************************************

clone 40     TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
clone 3      TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
clone 5      TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
             **************************************************

clone 40     ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
clone 3      ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
clone 5      ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
             **************************************************

clone 40     TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
clone 3      TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTTAT
clone 5      TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTTAT
             *********************************************** **

clone 40     TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
clone 3      TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
clone 5      TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
             **************************************************
```

Fig. 2 (Part 1 of 2)

```
clone 40      AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
clone 3       AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
clone 5       AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
              **************************************************

clone 40      GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
clone 3       GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
clone 5       GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
              **************************************************

clone 40      CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACC
clone 3       CTGGTAGATCTATCAGACCACTTTTATCAGCAGGACAACTGGTCGTTACC
clone 5       CTGGTAGATCTATCAGACCACTTTTATCAGCAGGACAACTGGTCGTTACC
              ****************** *******************************

clone 40      AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
clone 3       AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
clone 5       AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
              **************************************************

clone 40      ATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAAAA
clone 3       ATAGAATATTGAAAATAA--------------------------------
clone 5       ATAGAATATTGAAAATAAAATGTTAATAGACACTGGTTGAAA------AAA
              ******************

clone 40      AAAAAAAAAAAAAACTCGAG
clone 3       --------------------
clone 5       AAAAAAAAAAAAAACTCGAG
```

Fig. 2 (*Part 2 of 2*)

*GAATTCGGCACGAG*TCGGAAAAGAACAAA**ATGGCTTGTATCGTTTTCGT**TGCTCTTG
8S
TCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACAATGCGCGATGAATT

GGACACAAGCTAATGAATATGTGTTCAACGTGGACTGGATGACCATTTTCATCTACG

ACTATGGCGCTCAAGAGCAACTGTACGAAG**ATCGGGCTTTGGGGCTGTGT**CGGATTG
3A
AACGGGCCGGCCCAGGTACCACAAAAGCCGTCTGGATTAACTGGAGTAACGACACGC

AGTCATGTGTAACAAGAAAAACAATCTTCTTCGAGGTTGGTGGAGAAAT**TGCCCGGC**
4S
TAGTTGACTACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCT

CTAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGGACGCTG

ATGATAAA**TGCATCGAAGGCACAATTG**TGGTGACAGTCAGGGTGTCCCTATATGACG
6A
AAGATAACAATGGTGTAATGGATGAAGGTAAGGTGTTCCATCTGAGACAATCGAGGA

TGATATCAA**GGACTGTGGGCTCTTAG**ACCAAGATGTTGAACTCGATTATACGTGGAC
7S
TCAAAACGAGTGTGATCTACCAGACACAGTAGACGAGGCTGAAGACACACCGTCAGA

AACTGGAGAATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGG

TCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATC

GATAGAATATTGAAAATAAAATG**TTAATAAACACTGGTTGAAATATG**AAAAAAAAAA
5A
AAAAAAAA*CTCGAG*

Fig. 3

Untranslated region

*GAATTC*GGCACGAGTCGGAAAAGAACAAA

Translated region

```
ATG GCT TGT ATC GTT TTC GTT GCT CTT GTC GCT CTA TGC TTA ATG     45
M   A   C   I   V   F   V   A   L   V   A   L   C   L   M

CAA CCG GGT TCC GGT GAG GAA GTA CAA TGC GCG ATG AAT TGG ACA     90
Q   P   G   S   G   E   E   V   Q   C   A   M   N   W   T

CAA GCT AAT GAA TAT GTG TTC AAC GTG GAC TGG ATG ACC ATT TTC    135
Q   A   N   E   Y   V   F   N   V   D   W   M   T   I   F

ATC TAC GAC TAT GGC GCT CAA GAG CAA CTG TAC GAA GAT CGG GCT    180
I   Y   D   Y   G   A   Q   E   Q   L   Y   E   D   R   A

TTG GGG CTG TGT CGG ATT GAA CGG GCC GGC CCA GGT ACC ACA AAA    225
L   G   L   C   R   I   E   R   A   G   P   G   T   T   K

GCC GTC TGG ATT AAC TGG AGT AAC GAC ACG CAG TCA TGT GTA ACA    270
A   V   W   I   N   W   S   N   D   T   Q   S   C   V   T

AGA AAA ACA ATC TTC TTC GAG GTT GGT GGA GAA ATT GCC CGG CTA    315
R   K   T   I   F   F   E   V   G   G   E   I   A   R   L

GTT GAC TAC AGA CCA CAG GAA GAC GGA ACT GAG AAA ACT TTT ACA    360
V   D   Y   R   P   Q   E   D   G   T   E   K   T   F   T

AGA AAA TTC TCT AGC AAA ATG CCA GGC ACT TAC ATG CTT ATG GAC    405
R   K   F   S   S   K   M   P   G   T   Y   M   L   M   D

GTG TGC GCT ACA AGG GAC GCT GAT GAT AAA TGC ATC GAA GGC ACA    450
V   C   A   T   R   D   A   D   D   K   C   I   E   G   T

ATT GTG GTG ACA GTC AGG GTG TCC CTA TAT GAC GAA GAT AAC AAT    495
I   V   V   T   V   R   V   S   L   Y   D   E   D   N   N

GGT GTA ATG GAT GAA GGT AAG GTG ATT CCA TCT GAG ACA ATC GAG    540
G   V   M   D   E   G   K   V   I   P   S   E   T   I   E

GAT GAT ATC AAG GAC TGT GGG CTC TTA GAC CAA GAT GTT GAA CTC    585
D   D   I   K   D   C   G   L   L   D   Q   D   V   E   L

GAT TAT ACG TGG ACT CAA AAC GAG TGT GAT CTA CCA GAC ACA GTA    630
D   Y   T   W   T   Q   N   E   C   D   L   P   D   T   V

GAC GAG GCT GAA GAC ACA CCG TCA GAA ACT GGA GAA TTC TTC TGG    675
D   E   A   E   D   T   P   S   E   T   G   E   F   F   W

TAG ATC TAT CAG ACT ACT TTT ATC AGC AGG ACA ACT GGT CGT TAC    720
*

CAG ACA CCT ATA ACG TGT CCT CAT CAA TAA                        750
```

* = stop for translation

Fig. 4A

EcoR I

*GAATTCGGCACGAG*TCGGAAAAGAACAAA

ATG GCT TGT ATC GTT TTC GTT GCT CTT GTC GCT CTA
TGC TTA ATG CAA CCG GGT TCC GGT GAG GAA GTA CAA
TGC GCG ATG AAT TGG ACA CAA GCT AAT GAA TAT GTG
TTC AAC GTG GAC TGG ATG ACC ATT TTC ATC TAC GAC
TAT GGC GCT CAA GAG CAA CTG TAC GAA GAT CGG GCT
TTG GGG CTG TGT CGG ATT GAA CGG GCC GGC CCA GGT
ACC ACA AAA GCC GTC TGG ATT AAC TGG AGT AAC GAC
ACG CAG TCA TGT GTA ACA AGA AAA ACA ATC TTC TTC
GAG GTT GGT GGA GAA ATT GCC CGG CTA GTT GAC TAC
AGA CCA CAG GAA GAC GGA ACT GAG AAA ACT TTT ACA
AGA AAA TTC TCT AGC AAA ATG CCA GGC ACT TAC ATG
CTT ATG GAC GTG TGC GCT ACA AGG GAC GCT GAT GAT
AAA TGC ATC GAA GGC ACA ATT GTG GTG ACA GTC AGG
GTG TCC CTA TAT GAC GAA GAT AAC AAT GGT GTA ATG
GAT GAA GGT AAG GTG ATT CCA TCT GAG ACA ATC GAG
GAT GAT ATC AAG GAC TGT GGG CTC TTA GAC CAA GAT
GTT GAA CTC GAT TAT ACG TGG ACT CAA AAC GAG TGT
GAT CTA CCA GAC ACA GTA GAC GAG GCT GAA GAC ACA
CCG TCA GAA ACT GGA GAA TTC TTC TGG **TAG**

ATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACCAGAC
ACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCGA
TAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAA
AAAAAAAAAAAAAAAA*CTCGAG*

Xho I

Fig. 4B

EEVQCAMNWTQANEYVFNVDWMTIFIYDYGAQEQLYEDRALGLCRIERAGPGTTKAV
WINWSNDTQSCVTRKTIFFEVGGEIARLVDYRPQEDGTEKTFTRKFSSKMPGTYMLM
DVCATRDADDKCIEGTIVVTVRVSLYDEDNNGVMDEGKVIPSETIEDDIKDCGLLDQ
DVELDYTWTQNECDLPDTVDEAEDTPSETGEFFW

Fig. 5A

MACIVFVALVALCLMQPGSGEEVQCAMNWTQANEYVFNVDWMTIFIYDYGAQEQLYE
DRALGLCRIERAGPGTTKAVWINWSNDTQSCVTRKTIFFEVGGEIARLVDYRPQEDG
TEKTFTRKFSSKMPGTYMLMDVCATRDADDKCIEGTIVVTVRVSLYDEDNNGVMDEG
KVIPSETIEDDIKDCGLLDQDVELDYTWTQNECDLPDTVDEAEDTPSETGEFFW

Fig. 5B

```
clone 40    GAATTCGGCACGAGTCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT
BioXAct                                   TGGCTTGTATCGTTTTCGTT
rTth

clone 40    GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
BioXAct     GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
rTth                     TATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
                         *************************************

clone 40    ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
BioXAct     ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
rTth        ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
            **************************************************

clone 40    GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
BioXAct     GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
rTth        GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
            **************************************************

clone 40    GATCGGGCTTTGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCAC
BioXAct     GATCGGGCTTTGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCAC
rTth        GATCGGGCTTTGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCAC
            **************************************************

clone 40    AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
BioXAct     AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
rTth        AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
            **************************************************

clone 40    GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
BioXAct     GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
rTth        GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
            **************************************************

clone 40    TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC
BioXAct     TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC
rTth        TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC
            **************************************************

clone 40    TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
BioXAct     TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
rTth        TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
            **************************************************

clone 40    ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
BioXAct     ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
rTth        ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
            **************************************************

clone 40    TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
BioXAct     TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
rTth        TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
            **************************************************

clone 40    TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
BioXAct     TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
```

Fig. 6 ***(Part 1 of 2)***

```
rTth        TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
            **************************************************

clone 40    AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
BioXAct     AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
rTth        AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
            **************************************************

clone 40    GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
BioXAct     GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
rTth        GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
            **************************************************

clone 40    CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACC
BioXAct     CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACC
rTth        CTGGTANATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACC
            ****** *******************************************

clone 40    AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
BioXAct     AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
rTth        AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAAC
            ***************************************

clone 40    ATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAAAA
BioXAct     ATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAA
rTth

clone 40    AAAAAAAAAAAAAACTCGAG
BioXAct
rTth
```

Fig. 6 (Part 2 of 2)

Oligo 1

ACI ATH TTY TTY CAR GT

Oligo 2

CAR GAR GAR GGN ACI GA

Oligo 2A

TCI GTN CCY TCY TCY TG

Oligo N

TTY AAY GTI GAY TGG ATG

M=A/C R=A/G W=A/T S=G/C Y=C/T
K=G/T

V=A/C/G H=A/C/T D=A/G/T B=C/G/T N=A/C/G/T
I=inosine

Fig. 7A

Oligo 3A

ACA CAG CCC CAA AGC CCG AT

Oligo 4S

TTG CCC GGC TAG TTG ACT AC

Oligo 5A

CAT ATT TCA ACC AGT GTT TAT TAA

Oligo 6A

CAA TTG TGC CTT CGA TGC A

Oligo 7S

GGA CTG TGG GCT CTT AG

Oligo 8S

ATG GCT TGT ATC GTT TTC GT

Oligo T7

Fig. 7B

Oligo ExS

CCA CAC GGA TCC TGA GGA AGT ACA ATG

Oligo ExA

CCA CAC GGA TCC TTA TTG ATG AGG ACA

Oligo Bac1

CTT GTT TTT ATG GTC GTC TAC ATT TCT TAC ATC TAT GCG GAG
GAA GTA CAA TG

Oligo C9 12

CCA CAC AGA TCT AGA ATG AAA TTC TTA GTC AAC GTT GCC CTT
GTT TTT ATG GTC

Oligo BV5

TTT ACT GTT TTC GTA ACA GTT TTG

Oligo BV3

CAA CAA CGC ACA GAA TCT AG

Fig. 7C

AccI		630						
AflIII		405		734				
AluI 95								
AlwNI	659							
Asp 718		215						
AsuI		204	209					
BanI		215						
BanII		564						
BcnI		51	310					
BglII		678						
Bsp1 286		564						
BstNI		213		384				
BstUI	77							
Cfr10I	206							
Cfr13I	204		209					
DdeI		345		528		565		
DpnI		174		615		680		
EcoRI	665							
EcoRII	211		382					
EcoRV	547							
FokI		136		518		554		
HaeII		153						
HaeIII	206		210					
HgaI		431						
HhaI		77		152		413		
HincII		319						
HinfI		520		598				
HinP1I	75		150		411			
HpaII	50		57		207		310	
HphI	71		469		529			
KpnI		219						
MaeI		314		372				
MaeII		114		405		593		734
MaeIII	245		265		457		716	
MboII	182		274		277		347	
497	653		661					
MnlI	54		282		531		627	
750								
MseI	41		237					
NaeI	208							
NciI		51		310				
NlaIII	264	397						
NlaIV	55		217					
NsiI		440						
NspHI	397							
PleI	592							
RsaI	69		167		217			
Sau3AI	172	613	678					
Sau96I	204	209						
ScrFI	51	213	310	384				
SfaNI	428							
TaqI 288	441	537	585					
XhoII	678							

Fig. 8

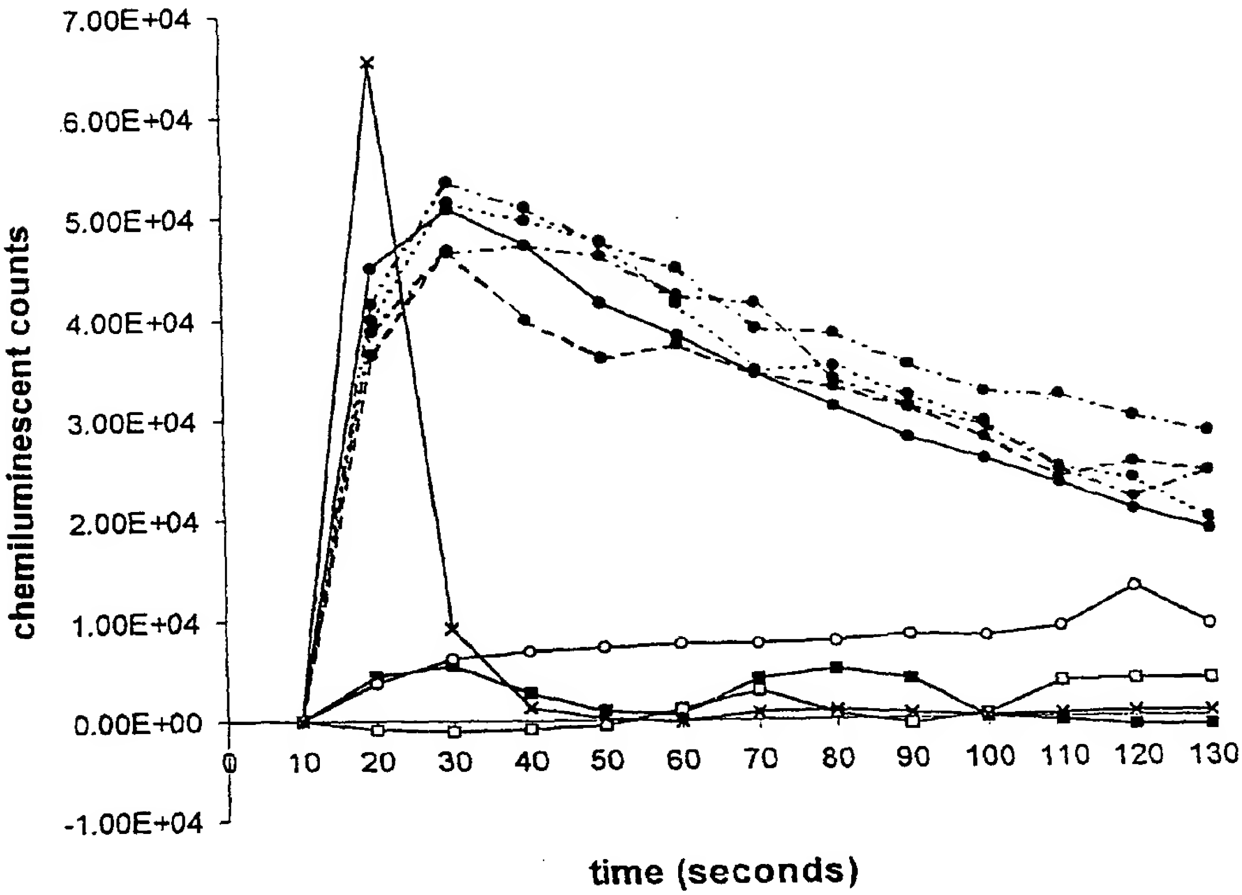
```
                                                                        NlaIV
                                                                       MnlI
                                                                    ScrFI
                                                                    NciI
                                                                    BcnI
                                                     MseI           HpaII   HpaII
                                                      |             ||   ||  |
    ATGGCTTGTATCGTTTTCGTTGCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGT      60

                       HhaI
                 HphI  BstUI
               RsaI  HinP1I              AluI                   MaeII
                | |   | |                 |                      |
GAGGAAGTACAATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGAC    120

                                   HaeII
                                  HhaI
                 FokI           HinP1I              RsaI  DpnI
                                                          Sau3AI
                  |               | ||               |    | |
TGGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAAGATCGGGCT    180

                                 HaeIII
                                Sau96I
                                Cfr13I
                               NaeI      RsaI
                              HpaII      NlaIV
                             HaeIII    BanI
                             Cfr10I  ScrFI
                           Sau96I    BstNI
                           Cfr13I EcoRII   KpnI
     MboII                 AsuI AsuI  Asp718                     MseI
      |                     | |||||| |  |  |  |                   |
TTGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCACAAAAGCCGTCTGGATTAAC    240

                             MaeIII      MboII
      MaeIII                NlaIII    MboII    MnlI   TaqI
        |                    ||         |  |      |       |
TGGAGTAACGACACGCAGTCATGTGTAACAAGAAAAACAATCTTCTTCGAGGTTGGTGGA    300

             MaeI
          ScrFI
          NciI
          HpaII                                          MboII
          BcnI      HincII                             DdeI
           |   |     |                                  | |
GAAATTGCCCGGCTAGTTGACTACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACA    360
```

Fig. 9 (Part 1 of 2)

```
                                 ScrFI
                                 BstNI           NspHI   MaeII HinPlI
                    MaeI       EcoRII            NlaIII  AflIII  HhaI
                     |         | |               |       |      | |
AGAAAATTCTCTAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGG   420

                   HgaI      TaqI
                SfaNI       NsiI                MaeIII      HphI
                |  |        ||                  |           |
GACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTGTCCCTATAT   480

                                                              MnlI
                                                  HinfI     HphI
                         MboII                  FokI      DdeI     TaqI
                         |                       | |        || |     |
GACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGATTCCATCTGAGACAATCGAG   540

                                  DdeI
                                Bsp1286                     MaeII
            EcoRV  FokI         BanII               TaqI   PleI  HinfI
            |      |            ||                  |      ||    |
GATGATATCAAGGACTGTGGGCTCTTAGACCAAGATGTTGAACTCGATTATACGTGGACT   600

                  DpnI           AccI
                Sau3AI         MnlI                       MboII  AlwNI
                | |            |  |                       |      |
CAAAACGAGTGTGATCTACCAGACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACT   660

                         DpnI
                       XhoII
          EcoRI        Sau3AI
      MboII            BglII                                 MaeIII
      |   |            | |                                   |
GGAGAATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTAC   720

                 MaeII
                 AflIII          MnlI
                 |               |
CAGACACCTATAACGTGTCCTCATCAATAA                                 750
```

Fig. 9 (Part 2 of 2)

FIGURE 10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6.00E+04
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-1.00E+04
chemiluminescent counts
0
10
20
30
40
50
60
70
80
90
100
110
120
130
time (seconds)